

# Matthew B Sullivan

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

|                    |                          |                 |                 |
|--------------------|--------------------------|-----------------|-----------------|
| 177<br>papers      | 18,234<br>citations      | 69<br>h-index   | 134<br>g-index  |
| 199<br>ext. papers | 25,754<br>ext. citations | 13.9<br>avg, IF | 6.77<br>L-index |

| #   | Paper   | IF   | Citations |
|-----|---|------|-----------|
| 177 | Life and death in the soil microbiome: how ecological processes influence biogeochemistry.. <i>Nature Reviews Microbiology</i> , <b>2022</b> ,                                      | 22.2 | 10        |
| 176 | MetaPop: a pipeline for macro- and microdiversity analyses and visualization of microbial and viral metagenome-derived populations.. <i>Microbiome</i> , <b>2022</b> , 10, 49       | 16.6 | 1         |
| 175 | Microbial metabolites in the marine carbon cycle.. <i>Nature Microbiology</i> , <b>2022</b> , 7, 508-523  | 26.6 | 2         |
| 174 | Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome.. <i>Science</i> , <b>2022</b> , 376, 156-162   | 33.3 | 9         |
| 173 | Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , <b>2022</b> , 2, 100123                    |      | 6         |
| 172 | The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , <b>2022</b> , 14, 973   | 6.2  | 0         |
| 171 | Coupling plant litter quantity to a novel metric for litter quality explains C storage changes in a thawing permafrost peatland. <i>Global Change Biology</i> , <b>2021</b> ,       | 11.4 | 2         |
| 170 | Viral community analysis in a marine oxygen minimum zone indicates increased potential for viral manipulation of microbial physiological state. <i>ISME Journal</i> , <b>2021</b> , | 11.9 | 2         |
| 169 | Friends or Foes? Rapid Determination of Dissimilar Colistin and Ciprofloxacin Antagonism of Phages. <i>Pharmaceuticals</i> , <b>2021</b> , 14,                                      | 5.2  | 2         |
| 168 | Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , <b>2021</b> , 6, 1561-1574                          | 26.6 | 9         |
| 167 | Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , <b>2021</b> , 51, 207-215   | 7.5  | 5         |
| 166 | Genome-resolved viral ecology in a marine oxygen minimum zone. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 2858-2874  | 5.2  | 4         |
| 165 | VirION2: a short- and long-read sequencing and informatics workflow to study the genomic diversity of viruses in nature. <i>PeerJ</i> , <b>2021</b> , 9, e11088                     | 3.1  | 8         |
| 164 | Revisiting the rules of life for viruses of microorganisms. <i>Nature Reviews Microbiology</i> , <b>2021</b> , 19, 501-513  | 22.2 | 14        |
| 163 | Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , <b>2021</b> , 4, 604                  | 6.7  | 17        |
| 162 | Viruses infecting a warm water picoeukaryote shed light on spatial co-occurrence dynamics of marine viruses and their hosts. <i>ISME Journal</i> , <b>2021</b> , 15, 3129-3147      | 11.9 | 2         |
| 161 | Improving Phage-Biofilm In Vitro Experimentation. <i>Viruses</i> , <b>2021</b> , 13,  | 6.2  | 5         |

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| 160 | Expanding standards in viromics: in silico evaluation of dsDNA viral genome identification, classification, and auxiliary metabolic gene curation. <i>PeerJ</i> , <b>2021</b> , 9, e11447 | 3.1  | 7  |
| 159 | Spinal Cord Injury Changes the Structure and Functional Potential of Gut Bacterial and Viral Communities. <i>MSystems</i> , <b>2021</b> , 6,  | 7.6  | 6  |
| 158 | Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. <i>Nature Communications</i> , <b>2021</b> , 12, 3503  | 17.4 | 12 |
| 157 | efam: an expanded, metaproteome-supported HMM profile database of viral protein families. <i>Bioinformatics</i> , <b>2021</b> ,   | 7.2  | 6  |
| 156 | Divergent Genomic Adaptations in the Microbiomes of Arctic Subzero Sea-Ice and Cryopeg Brines. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 701186                                | 5.7  | 1  |
| 155 | Glacier ice archives nearly 15,000-year-old microbes and phages. <i>Microbiome</i> , <b>2021</b> , 9, 160   | 16.6 | 7  |
| 154 | Potential virus-mediated nitrogen cycling in oxygen-depleted oceanic waters. <i>ISME Journal</i> , <b>2021</b> , 15, 981-998  | 11.9 | 13 |
| 153 | Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean. <i>IScience</i> , <b>2021</b> , 24, 102002  | 6.1  | 17 |
| 152 | Interaction dynamics and virus-host range for estuarine actinophages captured by epicPCR. <i>Nature Microbiology</i> , <b>2021</b> , 6, 630-642   | 26.6 | 10 |
| 151 | VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. <i>Microbiome</i> , <b>2021</b> , 9, 37   | 16.6 | 69 |
| 150 | Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. <i>Archives of Virology</i> , <b>2021</b> , 166, 3239-3244              | 2.6  | 5  |
| 149 | Environmental vulnerability of the global ocean epipelagic plankton community interactome. <i>Science Advances</i> , <b>2021</b> , 7,   | 14.3 | 5  |
| 148 | Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , <b>2021</b> , 11, 15714  | 4.9  | 2  |
| 147 | Diel cycle of sea spray aerosol concentration. <i>Nature Communications</i> , <b>2021</b> , 12, 5476  | 17.4 | 2  |
| 146 | High-throughput identification of viral termini and packaging mechanisms in virome datasets using PhageTermVirome. <i>Scientific Reports</i> , <b>2021</b> , 11, 18319                    | 4.9  | 0  |
| 145 | iVirus 2.0: Cyberinfrastructure-supported tools and data to power DNA virus ecology. <i>ISME Communications</i> , <b>2021</b> , 1,  |      | 1  |
| 144 | Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , <b>2020</b> , 18, 428-445  | 22.2 | 60 |
| 143 | Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , <b>2020</b> , 165, 1253-1260                   | 2.6  | 66 |

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| 142 | Unveiling Infection Strategies across Diverse Marine Phage-Host Systems. <i>Proceedings (mdpi)</i> , <b>2020</b> , 50, 99  | 0.3  |     |
| 141 | Viral Ecogenomics of Arctic Cryopeg Brine and Sea Ice. <i>MSystems</i> , <b>2020</b> , 5,  | 7.6  | 12  |
| 140 | Discovery of several thousand highly diverse circular DNA viruses. <i>ELife</i> , <b>2020</b> , 9,   | 8.9  | 65  |
| 139 | Author response: Discovery of several thousand highly diverse circular DNA viruses <b>2020</b> ,   |      | 5   |
| 138 | Metabolic and biogeochemical consequences of viral infection in aquatic ecosystems. <i>Nature Reviews Microbiology</i> , <b>2020</b> , 18, 21-34                                       | 22.2 | 97  |
| 137 | The spinal cord-gut-immune axis as a master regulator of health and neurological function after spinal cord injury. <i>Experimental Neurology</i> , <b>2020</b> , 323, 113085          | 5.7  | 26  |
| 136 | Phage-specific metabolic reprogramming of virocells. <i>ISME Journal</i> , <b>2020</b> , 14, 881-895   | 11.9 | 56  |
| 135 | The Gut Virome Database Reveals Age-Dependent Patterns of Virome Diversity in the Human Gut. <i>Cell Host and Microbe</i> , <b>2020</b> , 28, 724-740.e8                               | 23.4 | 125 |
| 134 | DRAM for distilling microbial metabolism to automate the curation of microbiome function. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 8883-8900                                  | 20.1 | 77  |
| 133 | Viral elements and their potential influence on microbial processes along the permanently stratified Cariaco Basin redoxcline. <i>ISME Journal</i> , <b>2020</b> , 14, 3079-3092       | 11.9 | 12  |
| 132 | Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. <i>Nature Ecology and Evolution</i> , <b>2020</b> , 4, 1639-1649                | 12.3 | 25  |
| 131 | Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , <b>2020</b> , 69, 110-123                                     | 8.4  | 56  |
| 130 | Future Ocean Observations to Connect Climate, Fisheries and Marine Ecosystems. <i>Frontiers in Marine Science</i> , <b>2019</b> , 6,   | 4.5  | 17  |
| 129 | The Tara Pacific expedition-A pan-ecosystemic approach of the "-omics" complexity of coral reef holobionts across the Pacific Ocean. <i>PLoS Biology</i> , <b>2019</b> , 17, e3000483  | 9.7  | 17  |
| 128 | ScientistsTwarning to humanity: microorganisms and climate change. <i>Nature Reviews Microbiology</i> , <b>2019</b> , 17, 569-586  | 22.2 | 516 |
| 127 | Soil Aggregate Microbial Communities: Towards Understanding Microbiome Interactions at Biologically Relevant Scales. <i>Applied and Environmental Microbiology</i> , <b>2019</b> , 85, | 4.8  | 126 |
| 126 | Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , <b>2019</b> , 177, 1109-1123.e14   | 56.2 | 256 |
| 125 | Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 632-639                            | 44.5 | 201 |

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| 124 | Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , <b>2019</b> , 33, 391-419  | 5.9  | 42  |
| 123 | Closely related viruses of the marine picoeukaryotic alga <i>Ostreococcus lucimarinus</i> exhibit different ecological strategies. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 2148-2170 | 5.2  | 11  |
| 122 | Numerous cultivated and uncultivated viruses encode ribosomal proteins. <i>Nature Communications</i> , <b>2019</b> , 10, 752   | 17.4 | 49  |
| 121 | Prevalence of viral photosynthesis genes along a freshwater to saltwater transect in Southeast USA. <i>Environmental Microbiology Reports</i> , <b>2019</b> , 11, 672-689                          | 3.7  | 10  |
| 120 | Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , <b>2019</b> , 179, 1068-1083.e21   | 56.2 | 113 |
| 119 | Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , <b>2019</b> , 179, 1084-1097.e21   | 56.2 | 108 |
| 118 | Long-read viral metagenomics captures abundant and microdiverse viral populations and their niche-defining genomic islands. <i>PeerJ</i> , <b>2019</b> , 7, e6800                                  | 3.1  | 68  |
| 117 | Optimizing genome assembly from PCR-amplified metagenomes. <i>PeerJ</i> , <b>2019</b> , 7, e6902   | 3.1  | 14  |
| 116 | Towards optimized viral metagenomes for double-stranded and single-stranded DNA viruses from challenging soils. <i>PeerJ</i> , <b>2019</b> , 7, e7265  | 3.1  | 26  |
| 115 | Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , <b>2019</b> , 37, 29-37   | 44.5 | 180 |
| 114 | Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing. <i>Nature Microbiology</i> , <b>2019</b> , 4, 352-361                                      | 26.6 | 49  |
| 113 | Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , <b>2018</b> , 9, 310                           | 17.4 | 55  |
| 112 | Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , <b>2018</b> , 163, 1125-1129                                 | 2.6  | 62  |
| 111 | A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , <b>2018</b> , 9, 373  | 17.4 | 168 |
| 110 | Multiple mechanisms drive phage infection efficiency in nearly identical hosts. <i>ISME Journal</i> , <b>2018</b> , 12, 1605-1618  | 11.9 | 28  |
| 109 | Clean Low-Biomass Procedures and Their Application to Ancient Ice Core Microorganisms. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1094  | 5.7  | 12  |
| 108 | Host-linked soil viral ecology along a permafrost thaw gradient. <i>Nature Microbiology</i> , <b>2018</b> , 3, 870-880   | 26.6 | 182 |
| 107 | Iron Chloride Flocculation of Bacteriophages from Seawater. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1681, 49-57  | 1.4  | 11  |

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| 106 | Whole-Genome Sequences of Phages p000v and p000y, Which Infect the Bacterial Pathogen Shiga-Toxigenic <i>Escherichia coli</i> . <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7, | 1.3  | 2   |
| 105 | Fighting Fire with Fire: Phage Potential for the Treatment of O157 Infection. <i>Antibiotics</i> , <b>2018</b> , 7,   | 4.9  | 7   |
| 104 | Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. <i>MSystems</i> , <b>2018</b> , 3,   | 7.6  | 99  |
| 103 | Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. <i>Nature Microbiology</i> , <b>2018</b> , 3, 1274-1284  | 26.6 | 70  |
| 102 | Smoking is associated with quantifiable differences in the human lung DNA virome and metabolome. <i>Respiratory Research</i> , <b>2018</b> , 19, 174  | 7.3  | 20  |
| 101 | Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. <i>ISME Journal</i> , <b>2017</b> , 11, 237-247  | 11.9 | 189 |
| 100 | Regulation of infection efficiency in a globally abundant marine Bacteriodes virus. <i>ISME Journal</i> , <b>2017</b> , 11, 284-295   | 11.9 | 33  |
| 99  | Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. <i>Microbiome</i> , <b>2017</b> , 5, 10                              | 16.6 | 595 |
| 98  | Modelling plankton ecosystems in the meta-omics era. Are we ready?. <i>Marine Genomics</i> , <b>2017</b> , 32, 1-17   | 1.9  | 23  |
| 97  | Single-virus genomics reveals hidden cosmopolitan and abundant viruses. <i>Nature Communications</i> , <b>2017</b> , 8, 15892   | 17.4 | 104 |
| 96  | Visualizing Adsorption of Cyanophage P-SSP7 onto Marine <i>Prochlorococcus</i> . <i>Scientific Reports</i> , <b>2017</b> , 7, 44176   | 4.9  | 15  |
| 95  | Lysogeny in nature: mechanisms, impact and ecology of temperate phages. <i>ISME Journal</i> , <b>2017</b> , 11, 1511-1520   | 11.9 | 272 |
| 94  | Consensus statement: Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , <b>2017</b> , 15, 161-168  | 22.2 | 375 |
| 93  | Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. <i>Nature Communications</i> , <b>2017</b> , 8, 858  | 17.4 | 62  |
| 92  | Dietary energy drives the dynamic response of bovine rumen viral communities. <i>Microbiome</i> , <b>2017</b> , 5, 155  | 16.6 | 38  |
| 91  | IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D457-D465   | 20.1 | 115 |
| 90  | Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. <i>MSphere</i> , <b>2017</b> , 2,   | 5    | 72  |
| 89  | Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , <b>2017</b> , 4, 170093  | 8.2  | 89  |

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| 88 | Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , <b>2017</b> , 162, 1153-1157                               | 2.6  | 38  |
| 87 | On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , <b>2017</b> , 8,   | 7.8  | 34  |
| 86 | iVirus: facilitating new insights in viral ecology with software and community data sets imbedded in a cyberinfrastructure. <i>ISME Journal</i> , <b>2017</b> , 11, 7-14                         | 11.9 | 80  |
| 85 | Viral ecology comes of age. <i>Environmental Microbiology Reports</i> , <b>2017</b> , 9, 33-35   | 3.7  | 45  |
| 84 | Comparative Omics and Trait Analyses of Marine Phages Advance the Phage OTU Concept. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1241  | 5.7  | 27  |
| 83 | vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect and. <i>PeerJ</i> , <b>2017</b> , 5, e3243  | 3.1  | 128 |
| 82 | Putative archaeal viruses from the mesopelagic ocean. <i>PeerJ</i> , <b>2017</b> , 5, e3428  | 3.1  | 36  |
| 81 | Benchmarking viromics: an evaluation of metagenome-enabled estimates of viral community composition and diversity. <i>PeerJ</i> , <b>2017</b> , 5, e3817   | 3.1  | 124 |
| 80 | Seasonal time bombs: dominant temperate viruses affect Southern Ocean microbial dynamics. <i>ISME Journal</i> , <b>2016</b> , 10, 437-49   | 11.9 | 168 |
| 79 | Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. <i>BMC Genomics</i> , <b>2016</b> , 17, 930  | 4.5  | 75  |
| 78 | Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , <b>2016</b> , 537, 689-693  | 50.4 | 400 |
| 77 | Illuminating structural proteins in viral "dark matter" with metaproteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 2436-41 | 11.5 | 49  |
| 76 | Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , <b>2016</b> , 532, 465-470  | 50.4 | 392 |
| 75 | Six Pseudoalteromonas Strains Isolated from Surface Waters of Kabeltonne, Offshore Helgoland, North Sea. <i>Genome Announcements</i> , <b>2016</b> , 4,  |      | 6   |
| 74 | Optimization of viral resuspension methods for carbon-rich soils along a permafrost thaw gradient. <i>PeerJ</i> , <b>2016</b> , 4, e1999   | 3.1  | 32  |
| 73 | Towards quantitative viromics for both double-stranded and single-stranded DNA viruses. <i>PeerJ</i> , <b>2016</b> , 4, e2777  | 3.1  | 108 |
| 72 | Large-scale maps of variable infection efficiencies in aquatic Bacteroidetes phage-host model systems. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 3949-3961                           | 5.2  | 18  |
| 71 | Depth-stratified functional and taxonomic niche specialization in the CoreTand FlexibleTPacific Ocean Virome. <i>ISME Journal</i> , <b>2015</b> , 9, 472-84                                      | 11.9 | 124 |

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|----|--|------|------|
| 70 | Viromes, not gene markers, for studying double-stranded DNA virus communities. <i>Journal of Virology</i> , <b>2015</b> , 89, 2459-61  | 6.6  | 41   |
| 69 | VirSorter: mining viral signal from microbial genomic data. <i>PeerJ</i> , <b>2015</b> , 3, e985   | 3.1  | 563  |
| 68 | Single-cell genomics-based analysis of virus-host interactions in marine surface bacterioplankton. <i>ISME Journal</i> , <b>2015</b> , 9, 2386-99  | 11.9 | 153  |
| 67 | Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 199   | 5.7  | 15   |
| 66 | Closing the gaps on the viral photosystem-I psaDCAB gene organization. <i>Environmental Microbiology</i> , <b>2015</b> , 17, 5100-8  | 5.2  | 6    |
| 65 | Variably lytic infection dynamics of large Bacteroidetes podovirus phi38:1 against two Cellulophaga baltica host strains. <i>Environmental Microbiology</i> , <b>2015</b> , 17, 4659-71  | 5.2  | 20   |
| 64 | Life-style and genome structure of marine Pseudoalteromonas siphovirus B8b isolated from the northwestern Mediterranean Sea. <i>PLoS ONE</i> , <b>2015</b> , 10, e0114829  | 3.7  | 10   |
| 63 | Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. <i>ELife</i> , <b>2015</b> , 4,  | 8.9  | 274  |
| 62 | An inexpensive, accurate, and precise wet-mount method for enumerating aquatic viruses. <i>Applied and Environmental Microbiology</i> , <b>2015</b> , 81, 2995-3000  | 4.8  | 16   |
| 61 | Ocean plankton. Determinants of community structure in the global plankton interactome. <i>Science</i> , <b>2015</b> , 348, 1262073  | 33.3 | 496  |
| 60 | Ocean plankton. Patterns and ecological drivers of ocean viral communities. <i>Science</i> , <b>2015</b> , 348, 1261498  | 33.3 | 421  |
| 59 | Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , <b>2015</b> , 348, 1261359   | 33.3 | 1261 |
| 58 | Ocean plankton. Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , <b>2015</b> , 348, 1261447   | 33.3 | 100  |
| 57 | Rising to the challenge: accelerated pace of discovery transforms marine virology. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 147-59   | 22.2 | 205  |
| 56 | Viral tagging reveals discrete populations in Synechococcus viral genome sequence space. <i>Nature</i> , <b>2014</b> , 513, 242-5  | 50.4 | 137  |
| 55 | Modeling ecological drivers in marine viral communities using comparative metagenomics and network analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 10714-9 | 11.5 | 79   |
| 54 | Emerging methods to study bacteriophage infection at the single-cell level. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 724  | 5.7  | 28   |
| 53 | Contrasting genomic patterns and infection strategies of two co-existing Bacteroidetes podovirus genera. <i>Environmental Microbiology</i> , <b>2014</b> , 16, 2501-13   | 5.2  | 28   |



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| 52 | Ecology and evolution of viruses infecting uncultivated SUP05 bacteria as revealed by single-cell- and meta-genomics. <i>ELife</i> , <b>2014</b> , 3, e03125  | 8.9  | 141 |
| 51 | Phage-bacteria infection networks. <i>Trends in Microbiology</i> , <b>2013</b> , 21, 82-91  | 12.4 | 200 |
| 50 | Sequencing platform and library preparation choices impact viral metagenomes. <i>BMC Genomics</i> , <b>2013</b> , 14, 320   | 4.5  | 77  |
| 49 | The global virome: not as big as we thought?. <i>Current Opinion in Virology</i> , <b>2013</b> , 3, 566-71  | 7.5  | 51  |
| 48 | Single-cell and population level viral infection dynamics revealed by phageFISH, a method to visualize intracellular and free viruses. <i>Environmental Microbiology</i> , <b>2013</b> , 15, 2306-18                                      | 5.2  | 95  |
| 47 | Preparation of metagenomic libraries from naturally occurring marine viruses. <i>Methods in Enzymology</i> , <b>2013</b> , 531, 143-65  | 1.7  | 26  |
| 46 | Evaluation of methods to concentrate and purify ocean virus communities through comparative, replicated metagenomics. <i>Environmental Microbiology</i> , <b>2013</b> , 15, 1428-40   | 5.2  | 122 |
| 45 | Abundant SAR11 viruses in the ocean. <i>Nature</i> , <b>2013</b> , 494, 357-60  | 50.4 | 238 |
| 44 | Global morphological analysis of marine viruses shows minimal regional variation and dominance of non-tailed viruses. <i>ISME Journal</i> , <b>2013</b> , 7, 1738-51  | 11.9 | 106 |
| 43 | Twelve previously unknown phage genera are ubiquitous in global oceans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 12798-803   | 11.5 | 140 |
| 42 | Metabolic reprogramming by viruses in the sunlit and dark ocean. <i>Genome Biology</i> , <b>2013</b> , 14, R123   | 18.3 | 137 |
| 41 | Contrasting Life Strategies of Viruses That Infect Photo- and Heterotrophic Bacteria, as Revealed by Viral Tagging. <i>MBio</i> , <b>2013</b> , 4,  | 7.8  | 3   |
| 40 | The Pacific Ocean virome (POV): a marine viral metagenomic dataset and associated protein clusters for quantitative viral ecology. <i>PLoS ONE</i> , <b>2013</b> , 8, e57355  | 3.7  | 256 |
| 39 | Phylogenomics of T4 cyanophages: lateral gene transfer in the TereTand origins of host genes. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 2113-26   | 5.2  | 84  |
| 38 | Towards quantitative metagenomics of wild viruses and other ultra-low concentration DNA samples: a rigorous assessment and optimization of the linker amplification method. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 2526-37 | 5.2  | 122 |
| 37 | Ocean viruses: rigorously evaluating the metagenomic sample-to-sequence pipeline. <i>Virology</i> , <b>2012</b> , 434, 181-6  | 3.6  | 72  |
| 36 | Contrasting life strategies of viruses that infect photo- and heterotrophic bacteria, as revealed by viral tagging. <i>MBio</i> , <b>2012</b> , 3,  | 7.8  | 72  |
| 35 | A simple and efficient method for concentration of ocean viruses by chemical flocculation. <i>Environmental Microbiology Reports</i> , <b>2011</b> , 3, 195-202   | 3.7  | 176 |

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| 34 | A simple and efficient method for concentration of ocean viruses by chemical flocculation. <i>Environmental Microbiology Reports</i> , <b>2011</b> , 3, 809-809                                  | 3.7  | 5    |
| 33 | Structural changes in a marine podovirus associated with release of its genome into <i>Prochlorococcus</i> . <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 830-6            | 17.6 | 121  |
| 32 | Genomic analysis of oceanic cyanobacterial myoviruses compared with T4-like myoviruses from diverse hosts and environments. <i>Environmental Microbiology</i> , <b>2010</b> , 12, 3035-56        | 5.2  | 237  |
| 31 | The genome and structural proteome of an ocean siphovirus: a new window into the cyanobacterial <i>Tribolium</i> . <i>Environmental Microbiology</i> , <b>2009</b> , 11, 2935-51                 | 5.2  | 97   |
| 30 | Portal protein diversity and phage ecology. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 2810-23  | 5.2  | 87   |
| 29 | Efficient phage-mediated pigment biosynthesis in oceanic cyanobacteria. <i>Current Biology</i> , <b>2008</b> , 18, 442-8   | 8.3  | 128  |
| 28 | Genome-wide expression dynamics of a marine virus and host reveal features of co-evolution. <i>Nature</i> , <b>2007</b> , 449, 83-6  | 50.4 | 248  |
| 27 | Community genomics among stratified microbial assemblages in the ocean's interior. <i>Science</i> , <b>2006</b> , 311, 496-503   | 33.3 | 1055 |
| 26 | Genomic islands and the ecology and evolution of <i>Prochlorococcus</i> . <i>Science</i> , <b>2006</b> , 311, 1768-70  | 33.3 | 362  |
| 25 | Prevalence and evolution of core photosystem II genes in marine cyanobacterial viruses and their hosts. <i>PLoS Biology</i> , <b>2006</b> , 4, e234  | 9.7  | 326  |
| 24 | Three <i>Prochlorococcus</i> cyanophage genomes: signature features and ecological interpretations. <i>PLoS Biology</i> , <b>2005</b> , 3, e144  | 9.7  | 411  |
| 23 | Transfer of photosynthesis genes to and from <i>Prochlorococcus</i> viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 11013-8 | 11.5 | 406  |
| 22 | Cyanophages infecting the oceanic cyanobacterium <i>Prochlorococcus</i> . <i>Nature</i> , <b>2003</b> , 424, 1047-51   | 50.4 | 393  |
| 21 | Genome divergence in two <i>Prochlorococcus</i> ecotypes reflects oceanic niche differentiation. <i>Nature</i> , <b>2003</b> , 424, 1042-7   | 50.4 | 904  |
| 20 | The IsoGenie database: an interdisciplinary data management solution for ecosystems biology and environmental research. <i>PeerJ</i> , 8, e9467  | 3.1  | 4    |
| 19 | In vitro analysis of colistin and ciprofloxacin antagonism of <i>Pseudomonas aeruginosa</i> phage PEV2 infection activities  |      | 1    |
| 18 | Glacier ice archives fifteen-thousand-year-old viruses   |      | 9    |
| 17 | DRAM for distilling microbial metabolism to automate the curation of microbiome function   |      | 6    |

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| 16 | Genome-resolved viral ecology in a marine oxygen minimum zone (OMZ)  | 1      |
| 15 | Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages  | 6      |
| 14 | VIRLON2: a short- and long-read sequencing and informatics workflow to study the genomic diversity of viruses in nature              | 2      |
| 13 | MetaPop: A pipeline for macro- and micro-diversity analyses and visualization of microbial and viral metagenome-derived populations  | 3      |
| 12 | Novel integrative elements and genomic plasticity in ocean ecosystems  | 7      |
| 11 | Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Bacteriophages                                  | 8      |
| 10 | Soil viruses are underexplored players in ecosystem carbon processing  | 3      |
| 9  | Long-read viral metagenomics enables capture of abundant and microdiverse viral populations and their niche-defining genomic islands | 3      |
| 8  | Gene sharing networks to automate genome-based prokaryotic viral taxonomy  | 9      |
| 7  | Discovery of several thousand highly diverse circular DNA viruses  | 5      |
| 6  | Metabolic Architecture of the Deep Ocean Microbiome  | 17     |
| 5  | The human gut virome database  | 27     |
| 4  | Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean   | 5      |
| 3  | Genomic evidence for global ocean plankton biogeography shaped by large-scale current systems  | 20     |
| 2  | Uncharted biosynthetic potential of the ocean microbiome   | 6      |
| 1  | Biosynthetic potential of the global ocean microbiome. <i>Nature</i> ,   | 50.4 6 |